RT-PCR   Purified RT-PCR product

RTPCR1

RTPCR2

~562bp
~501bp

Figure 1a

ZE   EC   NEC   YL

RTPCR1

RTPCR2

Figure 1b

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

~1995nt ⟶ 2370nt
1350nt

1 2 3 4 5 6 7 8 9 10 11 12 1314 15 161718
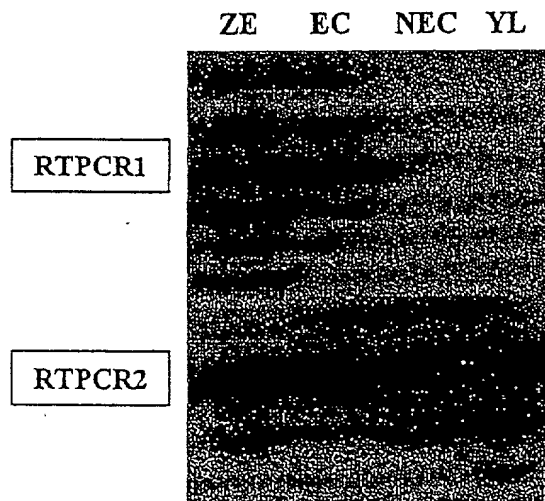
18S ⟶

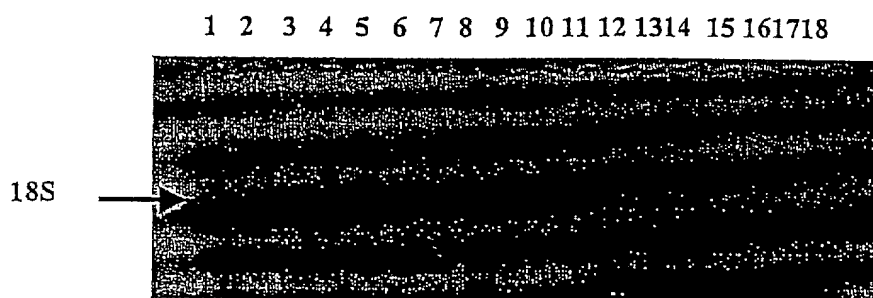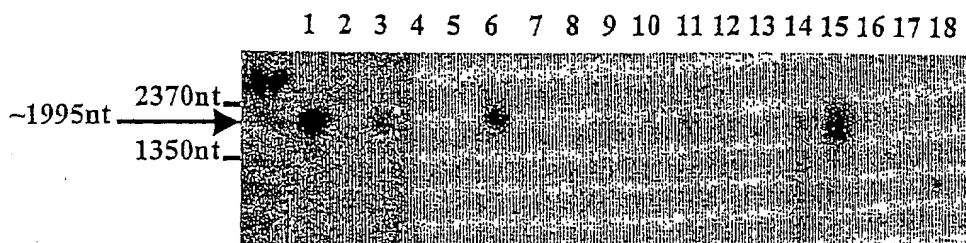Figure 2a

```
3    CAC GAG GTG AAT CGG AGC CGT TGA AAG ATG CCG GGG CTA ACG ATC    47
0                                        M   P   G   L   T   I   14

48   GGC GAC ACG ATC CCG AAC CTG GAG GTG GAG ACC ACG CAC GGG AAG    92
15   G   D   T   I   P   N   L   E   V   E   T   T   H   G   K    29

93   ATC CGG ATC CAC GAC TAC GTC GGC GAT GGT TGG GCC ATC ATC TTC    137
30   I   R   I   H   D   Y   V   G   D   G   W   A   I   I   F    44

138  TCC CAT CCC GCG GAT TTC ACA CCC GTG TGC ACG ACG GAG CTG GGG    182
45   S   H   P   A   D   F   T   P   V   C   T   T   E   L   G    59

183  AAG ATG GCG GCG TAC GCG GAG GAG TTC GAG AAA AGA GGG GTG AAG    227
60   K   M   A   A   Y   A   E   E   F   E   K   R   G   V   K    74

228  CTG CTA GGC ATC TCC TGC GAC GAT GTC AAG TGC CAC ATG GAA TGG    272
75   L   L   G   I   S   C   D   D   V   K   C   H   M   E   W    89

273  ATC AAA GAC GTC GAG GCC TAC ACG CCC GGA TGT CGC GTA ACA TAT    317
90   I   K   D   V   E   A   Y   T   P   G   C   R   V   T   Y    104

318  CCA ATT GTA GCC GAC CCC AAG AGG GAG GTG ATC AAA CTG CTG AAC    362
105  P   I   V   A   D   P   K   R   E   V   I   K   L   L   N    119

363  ATG GTA GAC CCT GAG GAG AAG GAC TCA AAT GGG AAC CAG CTC CCG    407
120  M   V   D   P   E   E   K   D   S   N   G   N   Q   L   P    134

408  TCA CGG GCC CTT CAT ATA GTG GGC CCT GAT AAG AAG GTT AAG CTG    452
135  S   R   A   L   H   I   V   G   P   D   K   K   V   K   L    149

453  AGC TTT CTG TAC CCG GCG TCG ACG GGG CGG AAC ATG GAG GAG GTG    497
150  S   F   L   Y   P   A   S   T   G   R   N   M   E   E   V    164

498  GTC AGG GTG TTG GAG TCG CTT CAG AAG ACG ATC AAG TAT AAG GTG    542
165  V   R   V   L   E   S   L   Q   K   T   I   K   Y   K   V    179

543  GCG ACC CCA GCG AAC TGG AAA CCG GGG GAG CCG GTG GTG ATC TCG    587
180  A   T   P   A   N   W   K   P   G   E   P   V   V   I   S    194

588  CCC GAG CGT GTC CAA TGA GGA GGC CAA GCA GAT GTT CCC GCA GGG    632
195  P   E   R   V   Q   *

633  AGT TGA GAA TGT GAA TCT CCC ATC GAA GAA GGA TTA CCT CCG CTT    677

678  CAC AAA AGT CTA ATG TTG TTG GGC CGT CCG TGA TAT GTT CAT AAG    722

723  TGG TTT CTG GGG CCC GAC TGT ATA CTG TGT TGT CGT GTT ATA TGT    767

768  TTG TGT TGG TAT CAT GTA GTT TGT GCC TTA GGG GAG TTT GGA TAT    812

813  TAA TTT GTA GTT TAT GTT AAT TAT TAA AGT TTT TAC CAT GAG ATT    857

858  AAA AAA AAA AAA AAA AAA    875
```

Figure 3
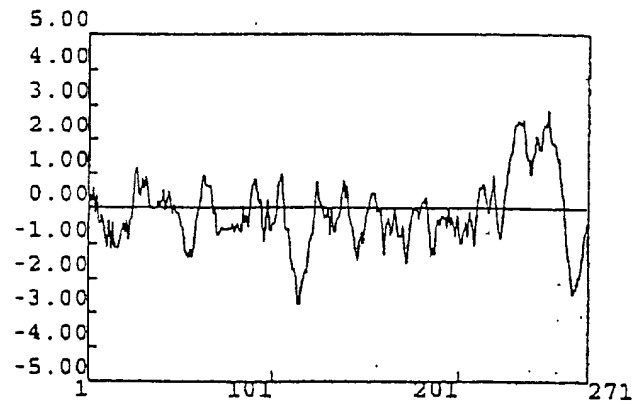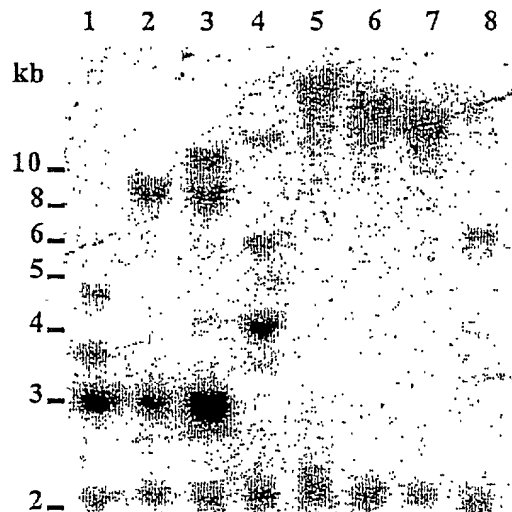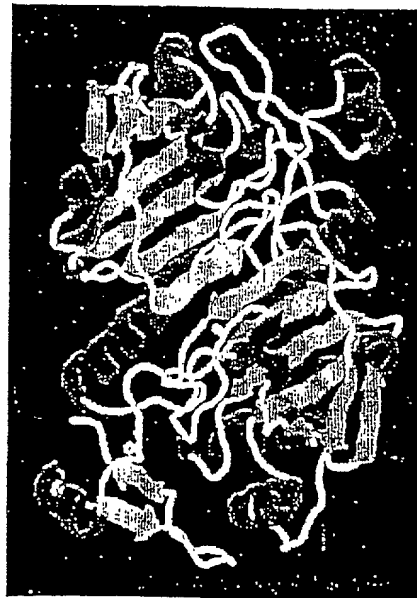
Figure 2b

Figure 2c
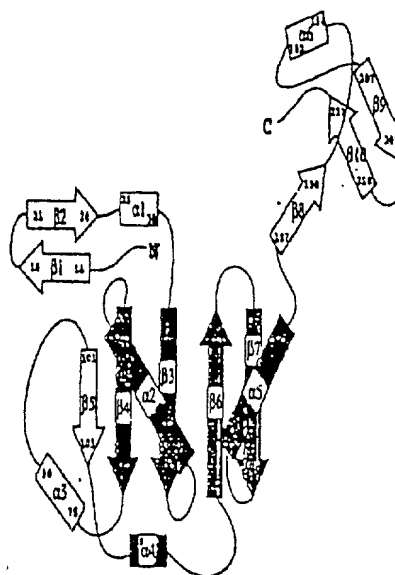
Figure 4a

Figure 4b

Figure 4c

Figure 4d

```
OPEm1       ------------------------------------MPGLT---------------------
HvPer1      ------------------------------------MPGLT---------------------
AtPer1      ------------------------------------MPGIT---------------------
C2CPRX      MASVASSTTLISSSASVLPATKSSLLPSPSLSFLPTLSSPSPSASLRSLVPLPSPQSASS
                                                 :*  ::


OPEm1       ----------------IGDTIPNLEVETTHG-------KIRIHDYVGDGWAIIFSHPADF
HvPer1      ----------------IGDTVPNLELDSTHG-------KIRIHDYVGNGYVILFSHPGDF
AtPer1      ----------------LGDTVPNLEVETTHD-------KFKLHDYFANSWTVLFSHPGDF
C2CPRX      SRRSFAVKGQTDDLPLVGNKAPDFEAEGVFDQEFIKFIKVKLSDYIGKKYVILFFLPLDF
                            :*:. *::* :  ...       *.:: **... :.::*   *  **


OPEm1       TPVCTTELGKMAAYAEEFEKRGVKLLGISCD--DVKCHMEWIKDVEAYTPGCRVTYPIVA
HvPer1      TPVCTTELAAMANYAKEFEKRGVKLLGISCD--DVQSHKEWTKDIBAYKPGSKVTYPIMA
AtPer1      TPVCTTELGAMAKYAHEFDKRGVKLLGLSCD--DVQSHKDWIKDIEAFNHGSKVNYPIIA
C2CPRX      TFVCPTEITAFSDRYAEFEKLNTEVLGVSVDSVSVFSHLAGVQTDRKFGGLGDLNYPLIS
            * **.**:  ::      **:*  ..::**:* *   .* .*      :   . .:       :..**::.


OPEm1       DPKREVIKLLNMVDPEEKDSNGNQLPSRALHIVGPDKKVKLSFLYPASTGRNMEEVVRVL
HvPer1      DPDRSAIKQLNMVDPDEKDAQG-QLPSRTLHIVGPDKVVKLSFLYPSCTGRNMDEVVRAV
AtPer1      DPNKEIIPQLNMIDPIE---NG---PSRALHIVGPDSKIKLSFLYPSTTGRNMDEVLRAL
C2CPRX      DVTKSISKSFGVLIHDQ----G--IALRGLFIIDKEGVIQHSTIN-LGIGRSVDETMRTL
            *  :.     :..::    :     *   . * *.*:. :   :: *.:   **.::*.:*.:


OPEm1       ESLQKTIKY--KVATPANWKPGEPVVISP----ERVQ-----------------------
HvPer1      DSLLTAAKH--KVATPANWKPGECVVIAPGVSDEEAKKMFPQGFETADLPSKKGYLRFTK
AtPer1      DSLLMASKHNNKIATPVNWKPDQPVVISPAVSDEEAKKMFPQGFKTADLPSKKGYLRHTE
C2CPRX      QALQYIQEGP-GEVCPAGWKPGEKSMKPDP---KLSKELFSAI-----------------
            ::*      :       . *..***.: . :  .       :  :


OPEm1       --
HvPer1      V-
AtPer1      VS
C2CPRX      --
```

Figure 5

```
OPEml    MPGLTIGDTIPNLEVETTHGKIRIHDYVGDGWAIIFSHPADFTPVCTTELGKMAAYAEEF
HvPerl   MPGLTIGDTVPNLELDSTHGKIRIHDYVGNGYVILFSHPGDFTPVCTTELAAMANYAKEF
AtPerl   MPGITLGDTVPNLEVETTHDKFKLHDYFANSWTVLFSHPGDFTPVCTTELGAMAKYAHEF
         ***:*:***:****::::**.*:::***..:.:.::****.**********. ** **.**


OPEml    EKRGVKLLGISCDDVKCHMEWIKDVEAYTPGCRVTYPIVADPKREVIKLLNMVDPEEKDS
HvPerl   EKRGVKLLGISCDDVQSHKEWTKDIEAYKPGSKVTYPIMADPDRSAIKQLNMVDPDEKDA
AtPerl   DKRGVKLLGLSCDDVQSHKDWIKDIEAFNHGSKVNYPIIADPNKEIIPQLNMIDPIE---
         :********:****:.* :* **:**:. *.:*.***:***.:. * ***:** *


OPEml    NGNQLPSRALHIVGPDKKVKLSFLYPASTGRNMEEVVRVLESLQKTIKY--KVATPANWK
HvPerl   QG-QLPSRTLHIVGPDKVVKLSFLYPSCTGRNMDEVVRAVDSLLTAAKH--KVATPANWK
AtPerl   NG---PSRALHIVGPDSKIKLSFLYPSTTGRNMDEVLRALDSLLMASKHNNKIATPVNWK
         :*    ***:*******. :*******: *****:**:*.::**   : *:  *:***.***


OPEml    PGEPVVISP----ERVQ-------------------------
HvPerl   PGECVVIAPGVSDEEAKKMFPQGFETADLPSKKGYLRFTKV-
AtPerl   PDQPVVISPAVSDEEAKKMFPQGFKTADLPSKKGYLRHTEVS
         *.: ***:*     *...:
```

Figure 6